FIGURE 1 (SHEET 1)

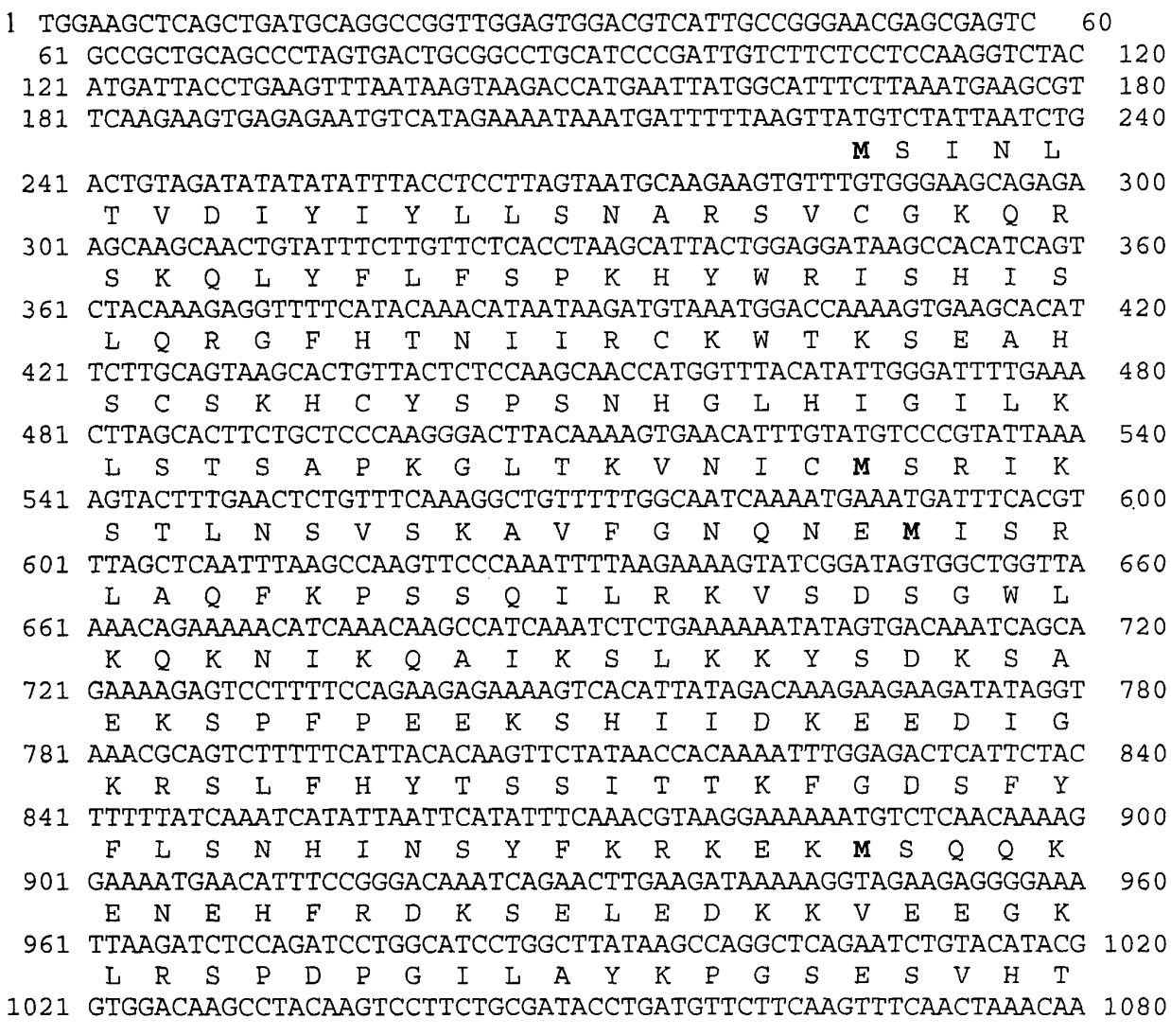


FIGURE 1 (SHEET 2)

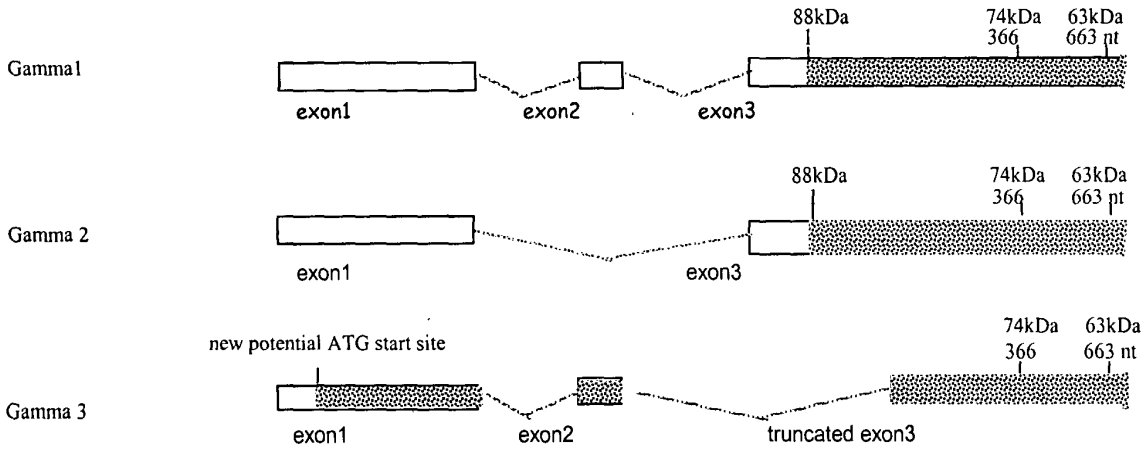
```
V  D  K  P  T  S  P  S  A  I  P  D  V  L  Q  V  S  T  K  Q
1081 AGTATTGCTAACTTTCTTTCTCGTCCCACGGAAGGTGTACAAGCTTTAGTAGGTGGTTAT 1140
     S  I  A  N  F  L  S  R  P  T  E  G  V  Q  A  L  V  G  G  Y
1141 ATTGGTGGACTTGTCCCCAAATTAAAGTATGATTCAAAGAGTCAGTCAGAAGAACAGGAA 1200
     I  G  G  L  V  P  K  L  K  Y  D  S  K  S  Q  S  E  E  Q  E
1201 GAGCCTGCTAAAACTGATCAGGCTGTCAGCAAAGACAGAAATGCAGAGGAGAAAAAGCGT 1260
     E  P  A  K  T  D  Q  A  V  S  K  D  R  N  A  E  E  K  K  R
1261 TTATCTCTTCAGCGAGAAAAGATTATCGCAAGGGTGAGTATTGATAACAGGACCCGGGCA 1320
     L  S  L  Q  R  E  K  I  I  A  R  V  S  I  D  N  R  T  R  A
1321 TTAGTTCAGGCATTAAGAAGAACAACTGACCCAAAGCTCTGCATTACTAGGGTTGAAGAA 1380
     L  V  Q  A  L  R  R  T  T  D  P  K  L  C  I  T  R  V  E  E
1381 CTGACTTTTCATCTTCTAGAATTTCCTGAAGGAAAAGGAGTGGCTGTCAAGGAAAGAATT 1440
     L  T  F  H  L  L  E  F  P  E  G  K  G  V  A  V  K  E  R  I
1441 ATTCCATATTTATTACGACTGAGACAAATTAAGGATGAAACTCTTCAGGCTGCAGTTAGA 1500
     I  P  Y  L  L  R  L  R  Q  I  K  D  E  T  L  Q  A  A  V  R
1501 GAAATTTTGGCCCTAATTGGCTATGTGGATCCAGTGAAAGGGAGAGGAATCCGAATTCTC 1560
     E  I  L  A  L  I  G  Y  V  D  P  V  K  G  R  G  I  R  I  L
1561 TCAATTGATGGTGGAGGAACAAGGGGCGTGGTTGCTCTCCAGACCCTACGAAAATTAGTT 1620
     S  I  D  G  G  G  T  R  G  V  V  A  L  Q  T  L  R  K  L  V
1621 GAACTTACTCAGAAGCCAGTTCATCAGCTCTTTGATTACATTTGTGGTGTAAGCACAGGT 1680
     E  L  T  Q  K  P  V  H  Q  L  F  D  Y  I  C  G  V  S  T  G
1681 GCCATATTAGCTTTCATGTTGGGGTTGTTTCATATGCCCTTGGATGAATGTGAGGAACTT 1740
     A  I  L  A  F  M  L  G  L  F  H  M  P  L  D  E  C  E  E  L
1741 TATCGAAAATTAGGATCAGATGTATTTTCACAAAATGTCATTGTTGGAACAGTAAAAATG 1800
     Y  R  K  L  G  S  D  V  F  S  Q  N  V  I  V  G  T  V  K  M
1801 AGTTGGAGCCATGCATTTTATGACAGTCAAACATGGGAAAACATTCTTAAGGATAGGATG 1860
     S  W  S  H  A  F  Y  D  S  Q  T  W  E  N  I  L  K  D  R  M
1861 GGATCTGCACTGATGATTGAAACAGCAAGAAACCCCACATGTCCTAAGGTAGCTGCTGTA 1920
     G  S  A  L  M  I  E  T  A  R  N  P  T  C  P  K  V  A  A  V
1921 AGTACCATAGTAAATAGAGGGATAACACCCAAAGCTTTTGTGTTCAGAAACTATGGTCAT 1980
     S  T  I  V  N  R  G  I  T  P  K  A  F  V  F  R  N  Y  G  H
1981 TTTCCTGGAATCAACTCTCATTATTTGGGAGGCTGTCAGTATAAAATGTGGCAGGCCATT 2040
     F  P  G  I  N  S  H  Y  L  G  G  C  Q  Y  K  M  W  Q  A  I
```

FIGURE 1 (SHEET 3)

```
2041 AGAGCCTCATCTGCTGCTCCAGGCTACTTTGCAGAATATGCATTGGGAAATGATCTTCAT 2100
      R  A  S  S  A  A  P  G  Y  F  A  E  Y  A  L  G  N  D  L  H
2101 CAAGATGGAGGTTTGCTTCTGAATAACCCTTCGGCATTAGCTATGCATGAGTGTAAATGT 2160
      Q  D  G  G  L  L  L  N  N  P  S  A  L  A  M  H  E  C  K  C
2161 CTTTGGCCAGATGTGCCGTTAGAGTGCATAGTATCCCTGGGCACTGGACGTTATGAGAGT 2220
      L  W  P  D  V  P  L  E  C  I  V  S  L  G  T  G  R  Y  E  S
2221 GATGTGAGAAACACGGTAACATACACAAGCTTGAAAACTAAACTTTCTAATGTTATCAAC 2280
      D  V  R  N  T  V  T  Y  T  S  L  K  T  K  L  S  N  V  I  N
2281 AGTGCTACAGATACAGAAGAAGTCCATATAATGCTTGATGGCCTGTTACCTCCTGACACC 2340
      S  A  T  D  T  E  E  V  H  I  M  L  D  G  L  L  P  P  D  T
2341 TATTTTAGATTCAATCCTGTAATGTGTGAAAACATACCTCTAGATGAAAGTCGAAATGAA 2400
      Y  F  R  F  N  P  V  M  C  E  N  I  P  L  D  E  S  R  N  E
2401 AAGCTGGATCAGCTGCAGTTGGAAGGGTTGAAATACATAGAAAGAAATGAACAAAAAATG 2460
      K  L  D  Q  L  Q  L  E  G  L  K  Y  I  E  R  N  E  Q  K  M
2461 AAAAAAGTTGCAAAAATATTAAGTCAAGAAAAAACAACTCTGCAGAAAATTAATGATTGG 2520
      K  K  V  A  K  I  L  S  Q  E  K  T  T  L  Q  K  I  N  D  W
2521 ATAAAATTAAAAACTGATATGTATGAAGGACTTCCATTCTTTTCAAAATTGTGATGAGTA 2580
      I  K  L  K  T  D  M  Y  E  G  L  P  F  F  S  K  L  -
2581 TATGCTTATGTTCTCATAAATGAAGGTCTGTTTAGAAGATCAACCACATTCAATAAGGAA 2640
2641 TTGTGGGGTTCGACATGAGTTAACTTTGAAATACGTATGAATTCTGGAGAATCCTGAAAA 2700
2701 AGACGGTGCTTCAACCAGCTTGCATAGCACAGAGAATATTCTTGGTTACAGAATTCATAT 2760
2761 GGGAACTAGGCTTTTAAGATGTTAATAATTAGCTAAGCTTTAGTAACCCTTACTGTGCTA 2820
2821 GTAGATTTTAGTAGATATTGGTGTTATATTGTTTGATGTTTGAAAATATATTAATATATG 2880
2881 TGCCGAACAAGAAACCGAAAGCTATATTGTACTGTGTATTTTTACTTTAGTCCTCATAAT 2940
2941 CATGTTGAATTTATGTGATCATTGATTTTATTTCATATGGAAAAGCTAATTTCTTCTTAA 3000
3001 ATTTACATTACCTAATATTCTCACTAGCTATGTTCTCCAATCCACACTGCCTTTTATTGT 3060
3061 AATATCATCTAAATAGATGCAGAAAAATGGAATTTTCTCTATTAAAGTATTTTACATTTG 3120
3121 ACATAAAAAAAGAACCAGATACAGTTTTCTATTCAGATATGTTTATTTTAACATTGTTTGG 3180
3180 TTAAAAAAGGTGAAGTTCCAGTCAACCACTTTTTACCCCTGAAATTTCAAGATAATGCTA 3240
3241 TATTAACTTTTCCAGATCTAACACTAGCTTATTCTTCCCTGTTATAAAATGGTTTGAACT 3300
3301 TACTGAGGAGATATTCCTATCATTAACAAAAATAAACTATTTAAATAATCTGTTGTTAAA 3360
3361 AGGCTAATGTCATTTTAAAATTAATTTTTGTTCATAATGTAGCTCCCCTTTAGCCTTTGA 3420
```

FIGURE 2

iPLA2γ Splice Variants



open boxes are noncoding regions
shaded regions are putative coding regions
stippled lines replresent intron splicing

FIGURE 3

Splice Variants of iPLA$_2\gamma$

4/5/00

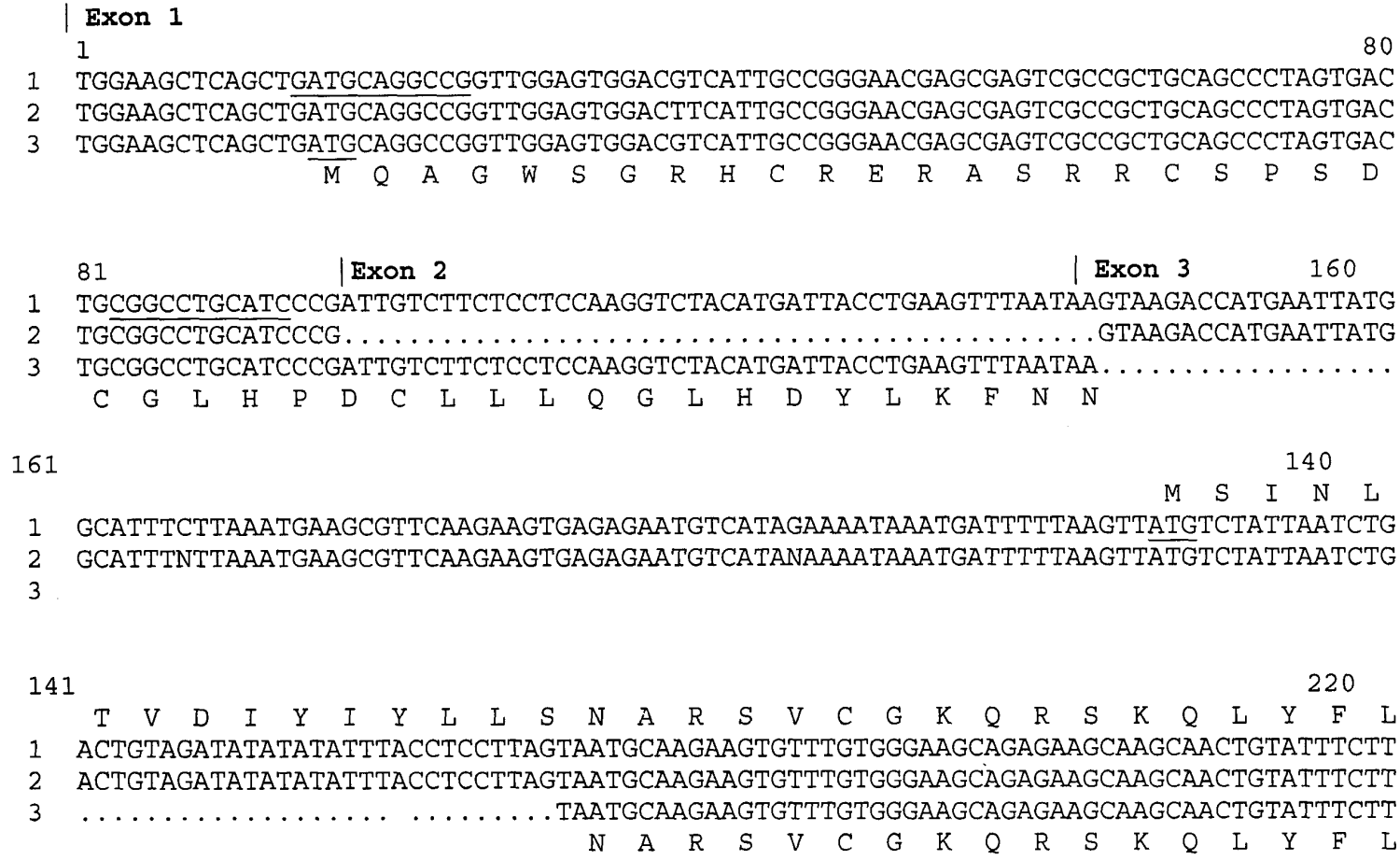


FIGURE 4 (SHEET 1)

Full-length iPLA2γ

Primers for PCR amplficiation of full-length 88kDa iPLA2γ:

Sense primer M444 5'-TTTTGTCGACATGTCTATTAATCTGACTGTAGATA-3'
Reverse primer M458 5'-GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3'

Sequence of 88kDa iPLA2 gamma:

```
atgtctattaatctgactgtagatatatatatttacctccttagtaatgcaagaagtgtt
 M  S  I  N  L  T  V  D  I  Y  I  Y  L  L  S  N  A  R  S  V
tgtgggaagcagagaagcaagcaactgtatttcttgttctcacctaagcattactggagg
 C  G  K  Q  R  S  K  Q  L  Y  F  L  F  S  P  K  H  Y  W  R
ataagccacatcagtctacaaagaggttttcatacaaacataataagatgtaaatggacc
 I  S  H  I  S  L  Q  R  G  F  H  T  N  I  I  R  C  K  W  T
aaaagtgaagcacattcttgcagtaagcactgttactctccaagcaaccatggtttacat
 K  S  E  A  H  S  C  S  K  H  C  Y  S  P  S  N  H  G  L  H
attgggattttgaaacttagcacttctgctcccaagggacttacaaaagtgaacatttgt
 I  G  I  L  K  L  S  T  S  A  P  K  G  L  T  K  V  N  I  C
atgtcccgtattaaaagtactttgaactctgtttcaaaggctgtttttggcaatcaaaat
 M  S  R  I  K  S  T  L  N  S  V  S  K  A  V  F  G  N  Q  N
gaaatgatttcacgtttagctcaatttaagccaagttcccaaattttaagaaaagtatcg
 E  M  I  S  R  L  A  Q  F  K  P  S  S  Q  I  L  R  K  V  S
gatagtggctggttaaaacagaaaaacatcaaacaagccatcaaatctctgaaaaaatat
 D  S  G  W  L  K  Q  K  N  I  K  Q  A  I  K  S  L  K  K  Y
agtgacaaatcagcagaaaagagtccttttccagaagagaaaagtcacattatagacaaa
 S  D  K  S  A  E  K  S  P  F  P  E  E  K  S  H  I  I  D  K
gaagaagatataggtaaacgcagtcttttcattacacaagttctataaccacaaaattt
 E  E  D  I  G  K  R  S  L  F  H  Y  T  S  S  I  T  T  K  F
ggagactcattctacttttttatcaaatcatattaattcatatttcaaacgtaaggaaaaa
 G  D  S  F  Y  F  L  S  N  H  I  N  S  Y  F  K  R  K  E  K
atgtctcaacaaaaggaaaatgaacatttccgggacaaatcagaacttgaagataaaaag
 M  S  Q  Q  K  E  N  E  H  F  R  D  K  S  E  L  E  D  K  K
```

FIGURE 4 (SHEET 2)

```
gtagaagaggggaaattaagatctccagatcctggcatcctggcttataagccaggctca
 V  E  E  G  K  L  R  S  P  D  P  G  I  L  A  Y  K  P  G  S
gaatctgtacatacggtggacaagcctacaagtccttctgcgatacctgatgttcttcaa
E  S  V  H  T  V  D  K  P  T  S  P  S  A  I  P  D  V  L  Q
gtttcaactaaacaaagtattgctaactttctttctcgtcccacggaaggtgtacaagct
V  S  T  K  Q  S  I  A  N  F  L  S  R  P  T  E  G  V  Q  A
ttagtaggtggttatattggtggacttgtccccaaattaaagtatgattcaaagagtcag
 L  V  G  G  Y  I  G  G  L  V  P  K  L  K  Y  D  S  K  S  Q
tcagaagaacaggaagagcctgctaaaactgatcaggctgtcagcaaagacagaaatgca
 S  E  E  Q  E  E  P  A  K  T  D  Q  A  V  S  K  D  R  N  A
gaggagaaaaagcgtttatctcttcagcgagaaaagattatcgcaagggtgagtattgat
 E  E  K  K  R  L  S  L  Q  R  E  K  I  I  A  R  V  S  I  D
aacaggacccgggcattagttcaggcattaagaagaacaactgacccaaagctctgcatt
 N  R  T  R  A  L  V  Q  A  L  R  R  T  T  D  P  K  L  C  I
actagggttgaagaactgacttttcatcttctagaatttcctgaaggaaaaggagtggct
 T  R  V  E  E  L  T  F  H  L  L  E  F  P  E  G  K  G  V  A
gtcaaggaaagaattattccatatttattacgactgagacaaattaaggatgaaactctt
 V  K  E  R  I  I  P  Y  L  L  R  L  R  Q  I  K  D  E  T  L
caggctgcagttagagaaattttggccctaattggctatgtggatccagtgaaagggaga
 Q  A  A  V  R  E  I  L  A  L  I  G  Y  V  D  P  V  K  G  R
ggaatccgaattctctcaattgatggtggaggaacaaggggcgtggttgctctccagacc
 G  I  R  I  L  S  I  D  G  G  G  T  R  G  V  V  A  L  Q  T
ctacgaaaattagttgaacttactcagaagccagttcatcagctctttgattacatttgt
 L  R  K  L  V  E  L  T  Q  K  P  V  H  Q  L  F  D  Y  I  C
ggtgtaagcacaggtgccatattagctttcatgttggggttgtttcatatgcccttggat
 G  V  S  T  G  A  I  L  A  F  M  L  G  L  F  H  M  P  L  D
gaatgtgaggaactttatcgaaaattaggatcagatgtattttcacaaaatgtcattgtt
 E  C  E  E  L  Y  R  K  L  G  S  D  V  F  S  Q  N  V  I  V
ggaacagtaaaaatgagttggagccatgcattttatgacagtcaaacatgggaaaacatt
 G  T  V  K  M  S  W  S  H  A  F  Y  D  S  Q  T  W  E  N  I
cttaaggataggatgggatctgcactgatgattgaaacagcaagaaaccccacatgtcct
 L  K  D  R  M  G  S  A  L  M  I  E  T  A  R  N  P  T  C  P
aaggtagctgctgtaagtaccatagtaaatagagggataacacccaaagcttttgtgttc
```

FIGURE 4 (SHEET 3)

```
 K  V  A  A  V  S  T  I  V  N  R  G  I  T  P  K  A  F  V  F
agaaactatggtcattttcctggaatcaactctcattatttgggaggctgtcagtataaa
 R  N  Y  G  H  F  P  G  I  N  S  H  Y  L  G  G  C  Q  Y  K
atgtggcaggccattagagcctcatctgctgctccaggctactttgcagaatatgcattg
 M  W  Q  A  I  R  A  S  S  A  A  P  G  Y  F  A  E  Y  A  L
ggaaatgatcttcatcaagatggaggtttgcttctgaataacccttcggcattagctatg
G  N  D  L  H  Q  D  G  G  L  L  L  N  N  P  S  A  L  A  M
catgagtgtaaatgtctttggccagatgtgccgttagagtgcatagtatccctgggcact
 H  E  C  K  C  L  W  P  D  V  P  L  E  C  I  V  S  L  G  T
ggacgttatgagagtgatgtgagaaacacggtaacatacacaagcttgaaaactaaactt
 G  R  Y  E  S  D  V  R  N  T  V  T  Y  T  S  L  K  T  K  L
tctaatgttatcaacagtgctacagatacagaagaagtccatataatgcttgatggcctg
 S  N  V  I  N  S  A  T  D  T  E  E  V  H  I  M  L  D  G  L
ttacctcctgacacctattttagattcaatcctgtaatgtgtgaaaacatacctctagat
 L  P  P  D  T  Y  F  R  F  N  P  V  M  C  E  N  I  P  L  D
gaaagtcgaaatgaaaagctggatcagctgcagttggaagggttgaaatacatagaaaga
 E  S  R  N  E  K  L  D  Q  L  Q  L  E  G  L  K  Y  I  E  R
aatgaacaaaaaatgaaaaaagttgcaaaaatattaagtcaagaaaaaacaactctgcag
 N  E  Q  K  M  K  K  V  A  K  I  L  S  Q  E  K  T  T  L  Q
aaaattaatgattggataaaattaaaaactgatatgtatgaaggacttccattcttttca
 K  I  N  D  W  I  K  L  K  T  D  M  Y  E  G  L  P  F  F  S
aaattgtga
 K  L  -
```

FIGURE 5 (SHEET 1)

Sequence of 77kDa iPLA2 gamma:
starting at amino acid 101 (nucleotide 301)

Primers for PCR amplficiation of 77kDa iPLA2γ:

Sense primer m534	5'-TGAACGTCGACATGTCCCGTATTAAAA-3'
Reverse primer M458	5'-GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3'

```
atgtcccgtattaaaagtactttgaactctgtttcaaaggctgtttttggcaatcaaaat
 M  S  R  I  K  S  T  L  N  S  V  S  K  A  V  F  G  N  Q  N
gaaatgatttcacgtttagctcaatttaagccaagttcccaaattttaagaaaagtatcg
 E  M  I  S  R  L  A  Q  F  K  P  S  S  Q  I  L  R  K  V  S
gatagtggctggttaaaacagaaaaacatcaaacaagccatcaaatctctgaaaaaatat
 D  S  G  W  L  K  Q  K  N  I  K  Q  A  I  K  S  L  K  K  Y
agtgacaaatcagcagaaaagagtccttttccagaagagaaaagtcacattatagacaaa
 S  D  K  S  A  E  K  S  P  F  P  E  E  K  S  H  I  I  D  K
gaagaagatataggtaaacgcagtcttttcattacacaagttctataaccacaaaattt
 E  E  D  I  G  K  R  S  L  F  H  Y  T  S  S  I  T  T  K  F
ggagactcattctacttttatcaaatcatattaattcatatttcaaacgtaaggaaaaa
 G  D  S  F  Y  F  L  S  N  H  I  N  S  Y  F  K  R  K  E  K
atgtctcaacaaaaggaaaatgaacatttccgggacaaatcagaacttgaagataaaaag
 M  S  Q  Q  K  E  N  E  H  F  R  D  K  S  E  L  E  D  K  K
gtagaagaggggaaattaagatctccagatcctggcatcctggcttataagccaggctca
 V  E  E  G  K  L  R  S  P  D  P  G  I  L  A  Y  K  P  G  S
gaatctgtacatacggtggacaagcctacaagtccttctgcgatacctgatgttcttcaa
 E  S  V  H  T  V  D  K  P  T  S  P  S  A  I  P  D  V  L  Q
gtttcaactaaacaaagtattgctaactttctttctcgtcccacggaaggtgtacaagct
 V  S  T  K  Q  S  I  A  N  F  L  S  R  P  T  E  G  V  Q  A
ttagtaggtggttatattggtggacttgtccccaaattaaagtatgattcaaagagtcag
 L  V  G  G  Y  I  G  G  L  V  P  K  L  K  Y  D  S  K  S  Q
tcagaagaacaggaagagcctgctaaaactgatcaggctgtcagcaaagacagaaatgca
 S  E  E  Q  E  E  P  A  K  T  D  Q  A  V  S  K  D  R  N  A
```

FIGURE 5 (SHEET 2)

```
gaggagaaaaagcgtttatctcttcagcgagaaaagattatcgcaagggtgagtattgat
 E  E  K  K  R  L  S  L  Q  R  E  K  I  I  A  R  V  S  I  D
aacaggacccgggcattagttcaggcattaagaagaacaactgacccaaagctctgcatt
N  R  T  R  A  L  V  Q  A  L  R  R  T  T  D  P  K  L  C  I
actagggttgaagaactgacttttcatcttctagaatttcctgaaggaaaaggagtggct
 T  R  V  E  E  L  T  F  H  L  L  E  F  P  E  G  K  G  V  A
gtcaaggaaagaattattccatatttattacgactgagacaaattaaggatgaaactctt
 V  K  E  R  I  I  P  Y  L  L  R  L  R  Q  I  K  D  E  T  L
caggctgcagttagagaaattttggccctaattggctatgtggatccagtgaaagggaga
 Q  A  A  V  R  E  I  L  A  L  I  G  Y  V  D  P  V  K  G  R
ggaatccgaattctctcaattgatggtggaggaacaaggggcgtggttgctctccagacc
 G  I  R  I  L  S  I  D  G  G  G  T  R  G  V  V  A  L  Q  T
ctacgaaaattagttgaacttactcagaagccagttcatcagctctttgattacatttgt
 L  R  K  L  V  E  L  T  Q  K  P  V  H  Q  L  F  D  Y  I  C
ggtgtaagcacaggtgccatattagctttcatgttggggttgtttcatatgcccttggat
 G  V  S  T  G  A  I  L  A  F  M  L  G  L  F  H  M  P  L  D
gaatgtgaggaactttatcgaaaattaggatcagatgtattttcacaaaatgtcattgtt
 E  C  E  E  L  Y  R  K  L  G  S  D  V  F  S  Q  N  V  I  V
ggaacagtaaaaatgagttggagccatgcattttatgacagtcaaacatgggaaaacatt
 G  T  V  K  M  S  W  S  H  A  F  Y  D  S  Q  T  W  E  N  I
cttaaggataggatgggatctgcactgatgattgaaacagcaagaaaccccacatgtcct
 L  K  D  R  M  G  S  A  L  M  I  E  T  A  R  N  P  T  C  P
aaggtagctgctgtaagtaccatagtaaatagagggataacacccaaagcttttgtgttc
 K  V  A  A  V  S  T  I  V  N  R  G  I  T  P  K  A  F  V  F
agaaactatggtcattttcctggaatcaactctcattatttgggaggctgtcagtataaa
 R  N  Y  G  H  F  P  G  I  N  S  H  Y  L  G  G  C  Q  Y  K
atgtggcaggccattagagcctcatctgctgctccaggctactttgcagaatatgcattg
 M  W  Q  A  I  R  A  S  S  A  A  P  G  Y  F  A  E  Y  A  L
ggaaatgatcttcatcaagatggaggtttgcttctgaataacccttcggcattagctatg
 G  N  D  L  H  Q  D  G  G  L  L  L  N  N  P  S  A  L  A  M
catgagtgtaaatgtctttggccagatgtgccgttagagtgcatagtatccctgggcact
 H  E  C  K  C  L  W  P  D  V  P  L  E  C  I  V  S  L  G  T
ggacgttatgagagtgatgtgagaaacacggtaacatacacaagcttgaaaactaaactt
```

FIGURE 5 (SHEET 3)

```
 G  R  Y  E  S  D  V  R  N  T  V  T  Y  T  S  L  K  T  K  L
tctaatgttatcaacagtgctacagatacagaagaagtccatataatgcttgatggcctg
 S  N  V  I  N  S  A  T  D  T  E  E  V  H  I  M  L  D  G  L
ttacctcctgacacctattttagattcaatcctgtaatgtgtgaaaacatacctctagat
 L  P  P  D  T  Y  F  R  F  N  P  V  M  C  E  N  I  P  L  D
gaaagtcgaaatgaaaagctggatcagctgcagttggaagggttgaaatacatagaaaga
 E  S  R  N  E  K  L  D  Q  L  Q  L  E  G  L  K  Y  I  E  R
aatgaacaaaaaatgaaaaaagttgcaaaaatattaagtcaagaaaaaacaactctgcag
 N  E  Q  K  M  K  K  V  A  K  I  L  S  Q  E  K  T  T  L  Q
aaaattaatgattggataaaattaaaaactgatatgtatgaaggacttccattcttttca
 K  I  N  D  W  I  K  L  K  T  D  M  Y  E  G  L  P  F  F  S
aaattgtga
 K  L  -
```

FIGURE 6 (SHEET 1)

Sequence of 74kDa iPLA2 gamma:
starting at amino acid 122 (nucleotide 364)

Primers for PCR amplfication of 74kDa iPLA2γ:

Sense primer m533 5'- TCAAGTCGACATGATTTCACGTTTAGC -3'
Reverse primer M458 5'-GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3'

```
atgatttcacgtttagctcaatttaagccaagttcccaaattttaagaaaagtatcg
 M  I  S  R  L  A  Q  F  K  P  S  S  Q  I  L  R  K  V  S
gatagtggctggttaaaacagaaaaacatcaaacaagccatcaaatctctgaaaaaatat
 D  S  G  W  L  K  Q  K  N  I  K  Q  A  I  K  S  L  K  K  Y
agtgacaaatcagcagaaaagagtccttttccagaagagaaaagtcacattatagacaaa
 S  D  K  S  A  E  K  S  P  F  P  E  E  K  S  H  I  I  D  K
gaagaagatataggtaaacgcagtctttttcattacacaagttctataaccacaaaattt
 E  E  D  I  G  K  R  S  L  F  H  Y  T  S  S  I  T  T  K  F
ggagactcattctacttttttatcaaatcatattaattcatatttcaaacgtaaggaaaaa
 G  D  S  F  Y  F  L  S  N  H  I  N  S  Y  F  K  R  K  E  K
atgtctcaacaaaaggaaaatgaacatttccgggacaaatcagaacttgaagataaaaag
 M  S  Q  Q  K  E  N  E  H  F  R  D  K  S  E  L  E  D  K  K
gtagaagaggggaaattaagatctccagatcctggcatcctggcttataagccaggctca
 V  E  E  G  K  L  R  S  P  D  P  G  I  L  A  Y  K  P  G  S
gaatctgtacatacggtggacaagcctacaagtccttctgcgatacctgatgttcttcaa
 E  S  V  H  T  V  D  K  P  T  S  P  S  A  I  P  D  V  L  Q
gtttcaactaaacaaagtattgctaactttctttctcgtcccacggaaggtgtacaagct
 V  S  T  K  Q  S  I  A  N  F  L  S  R  P  T  E  G  V  Q  A
ttagtaggtggttatattggtggacttgtccccaaattaaagtatgattcaaagagtcag
 L  V  G  G  Y  I  G  G  L  V  P  K  L  K  Y  D  S  K  S  Q
tcagaagaacaggaagagcctgctaaaactgatcaggctgtcagcaaagacagaaatgca
 S  E  E  Q  E  E  P  A  K  T  D  Q  A  V  S  K  D  R  N  A
gaggagaaaaagcgtttatctcttcagcgagaaaagattatcgcaagggtgagtattgat
 E  E  K  K  R  L  S  L  Q  R  E  K  I  I  A  R  V  S  I  D
```

FIGURE 6 (SHEET 2)

```
aacaggacccgggcattagttcaggcattaagaagaacaactgacccaaagctctgcatt
 N  R  T  R  A  L  V  Q  A  L  R  R  T  T  D  P  K  L  C  I
actagggttgaagaactgacttttcatcttctagaatttcctgaaggaaaaggagtggct
T  R  V  E  E  L  T  F  H  L  L  E  F  P  E  G  K  G  V  A
gtcaaggaaagaattattccatatttattacgactgagacaaattaaggatgaaactctt
 V  K  E  R  I  I  P  Y  L  L  R  L  R  Q  I  K  D  E  T  L
caggctgcagttagagaaattttggccctaattggctatgtggatccagtgaaagggaga
 Q  A  A  V  R  E  I  L  A  L  I  G  Y  V  D  P  V  K  G  R
ggaatccgaattctctcaattgatggtggaggaacaaggggcgtggttgctctccagacc
 G  I  R  I  L  S  I  D  G  G  G  T  R  G  V  V  A  L  Q  T
ctacgaaaattagttgaacttactcagaagccagttcatcagctctttgattacatttgt
 L  R  K  L  V  E  L  T  Q  K  P  V  H  Q  L  F  D  Y  I  C
ggtgtaagcacaggtgccatattagctttcatgttggggttgtttcatatgcccttggat
 G  V  S  T  G  A  I  L  A  F  M  L  G  L  F  H  M  P  L  D
gaatgtgaggaactttatcgaaaattaggatcagatgtattttcacaaaatgtcattgtt
 E  C  E  E  L  Y  R  K  L  G  S  D  V  F  S  Q  N  V  I  V
ggaacagtaaaaatgagttggagccatgcattttatgacagtcaaacatgggaaaacatt
 G  T  V  K  M  S  W  S  H  A  F  Y  D  S  Q  T  W  E  N  I
cttaaggataggatgggatctgcactgatgattgaaacagcaagaaaccccacatgtcct
 L  K  D  R  M  G  S  A  L  M  I  E  T  A  R  N  P  T  C  P
aaggtagctgctgtaagtaccatagtaaatagagggataacacccaaagcttttgtgttc
 K  V  A  A  V  S  T  I  V  N  R  G  I  T  P  K  A  F  V  F
agaaactatggtcattttcctggaatcaactctcattatttgggaggctgtcagtataaa
 R  N  Y  G  H  F  P  G  I  N  S  H  Y  L  G  G  C  Q  Y  K
atgtggcaggccattagagcctcatctgctgctccaggctactttgcagaatatgcattg
 M  W  Q  A  I  R  A  S  S  A  A  P  G  Y  F  A  E  Y  A  L
ggaaatgatcttcatcaagatggaggtttgcttctgaataacccttcggcattagctatg
 G  N  D  L  H  Q  D  G  G  L  L  L  N  N  P  S  A  L  A  M
catgagtgtaaatgtctttggccagatgtgccgttagagtgcatagtatccctgggcact
 H  E  C  K  C  L  W  P  D  V  P  L  E  C  I  V  S  L  G  T
ggacgttatgagagtgatgtgagaaacacggtaacatacacaagcttgaaaactaaactt
 G  R  Y  E  S  D  V  R  N  T  V  T  Y  T  S  L  K  T  K  L
tctaatgttatcaacagtgctacagatacagaagaagtccatataatgcttgatggcctg
```

FIGURE 6 (SHEET 3)

```
 S  N  V  I  N  S  A  T  D  T  E  E  V  H  I  M  L  D  G  L
ttacctcctgacacctattttagattcaatcctgtaatgtgtgaaaacatacctctagat
 L  P  P  D  T  Y  F  R  F  N  P  V  M  C  E  N  I  P  L  D
gaaagtcgaaatgaaaagctggatcagctgcagttggaagggttgaaatacatagaaaga
 E  S  R  N  E  K  L  D  Q  L  Q  L  E  G  L  K  Y  I  E  R
aatgaacaaaaaatgaaaaaagttgcaaaaatattaagtcaagaaaaaacaactctgcag
N  E  Q  K  M  K  K  V  A  K  I  L  S  Q  E  K  T  T  L  Q
aaaattaatgattggataaaattaaaaactgatatgtatgaaggacttccattcttttca
 K  I  N  D  W  I  K  L  K  T  D  M  Y  E  G  L  P  F  F  S
aaattgtga
 K  L  -
```

FIGURE 7 (SHEET 1)

Sequence of 63kDa iPLA2 gamma
starting at amino acid 221 (nucleotide 661)

Sense primer M530 5'-:GTAAGTCGACAATGTCTCAACAAAAGG-3'
Reverse primer M458 5'GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3')

```
atgtctcaacaaaaggaaaatgaacatttccgggacaaatcagaacttgaagataaaaag
 M  S  Q  Q  K  E  N  E  H  F  R  D  K  S  E  L  E  D  K  K
gtagaagaggggaaattaagatctccagatcctggcatcctggcttataagccaggctca
 V  E  E  G  K  L  R  S  P  D  P  G  I  L  A  Y  K  P  G  S
gaatctgtacatacggtggacaagcctacaagtccttctgcgatacctgatgttcttcaa
 E  S  V  H  T  V  D  K  P  T  S  P  S  A  I  P  D  V  L  Q
gtttcaactaaacaaagtattgctaactttctttctcgtcccacggaaggtgtacaagct
 V  S  T  K  Q  S  I  A  N  F  L  S  R  P  T  E  G  V  Q  A
ttagtaggtggttatattggtggacttgtccccaaattaaagtatgattcaaagagtcag
 L  V  G  G  Y  I  G  G  L  V  P  K  L  K  Y  D  S  K  S  Q
tcagaagaacaggaagagcctgctaaaactgatcaggctgtcagcaaagacagaaatgca
 S  E  E  Q  E  E  P  A  K  T  D  Q  A  V  S  K  D  R  N  A
gaggagaaaaagcgtttatctcttcagcgagaaaagattatcgcaagggtgagtattgat
 E  E  K  K  R  L  S  L  Q  R  E  K  I  I  A  R  V  S  I  D
aacaggacccgggcattagttcaggcattaagaagaacaactgacccaaagctctgcatt
 N  R  T  R  A  L  V  Q  A  L  R  R  T  T  D  P  K  L  C  I
actagggttgaagaactgacttttcatcttctagaatttcctgaaggaaaaggagtggct
 T  R  V  E  E  L  T  F  H  L  L  E  F  P  E  G  K  G  V  A
gtcaaggaaagaattattccatatttattacgactgagacaaattaaggatgaaactctt
 V  K  E  R  I  I  P  Y  L  L  R  L  R  Q  I  K  D  E  T  L
caggctgcagttagagaaattttggccctaattggctatgtggatccagtgaaagggaga
 Q  A  A  V  R  E  I  L  A  L  I  G  Y  V  D  P  V  K  G  R
ggaatccgaattctctcaattgatggtggaggaacaaggggcgtggttgctctccagacc
 G  I  R  I  L  S  I  D  G  G  G  T  R  G  V  V  A  L  Q  T
ctacgaaaattagttgaacttactcagaagccagttcatcagctctttgattacatttgt
 L  R  K  L  V  E  L  T  Q  K  P  V  H  Q  L  F  D  Y  I  C
```

FIGURE 7 (SHEET 2)

```
ggtgtaagcacaggtgccatattagctttcatgttggggttgtttcatatgcccttggat
 G  V  S  T  G  A  I  L  A  F  M  L  G  L  F  H  M  P  L  D
gaatgtgaggaactttatcgaaaattaggatcagatgtattttcacaaaatgtcattgtt
 E  C  E  E  L  Y  R  K  L  G  S  D  V  F  S  Q  N  V  I  V
ggaacagtaaaaatgagttggagccatgcattttatgacagtcaaacatgggaaaacatt
 G  T  V  K  M  S  W  S  H  A  F  Y  D  S  Q  T  W  E  N  I
cttaaggataggatgggatctgcactgatgattgaaacagcaagaaaccccacatgtcct
 L  K  D  R  M  G  S  A  L  M  I  E  T  A  R  N  P  T  C  P
aaggtagctgctgtaagtaccatagtaaatagagggataacacccaaagcttttgtgttc
 K  V  A  A  V  S  T  I  V  N  R  G  I  T  P  K  A  F  V  F
agaaactatggtcattttcctggaatcaactctcattatttgggaggctgtcagtataaa
 R  N  Y  G  H  F  P  G  I  N  S  H  Y  L  G  G  C  Q  Y  K
atgtggcaggccattagagcctcatctgctgctccaggctactttgcagaatatgcattg
 M  W  Q  A  I  R  A  S  S  A  A  P  G  Y  F  A  E  Y  A  L
ggaaatgatcttcatcaagatggaggtttgcttctgaataacccttcggcattagctatg
 G  N  D  L  H  Q  D  G  G  L  L  L  N  N  P  S  A  L  A  M
catgagtgtaaatgtctttggccagatgtgccgttagagtgcatagtatccctgggcact
 H  E  C  K  C  L  W  P  D  V  P  L  E  C  I  V  S  L  G  T
ggacgttatgagagtgatgtgagaaacacggtaacatacacaagcttgaaaactaaactt
 G  R  Y  E  S  D  V  R  N  T  V  T  Y  T  S  L´ K  T  K  L
tctaatgttatcaacagtgctacagatacagaagaagtccatataatgcttgatggcctg
 S  N  V  I  N  S  A  T  D  T  E  E  V  H  I  M  L  D  G  L
ttacctcctgacacctattttagattcaatcctgtaatgtgtgaaaacatacctctagat
 L  P  P  D  T  Y  F  R  F  N  P  V  M  C  E  N  I  P  L  D
gaaagtcgaaatgaaaagctggatcagctgcagttggaagggttgaaatacatagaaaga
 E  S  R  N  E  K  L  D  Q  L  Q  L  E  G  L  K  Y  I  E  R
aatgaacaaaaaatgaaaaaagttgcaaaaatattaagtcaagaaaaaacaactctgcag
 N  E  Q  K  M  K  K  V  A  K  I  L  S  Q  E  K  T  T  L  Q
aaaattaatgattggataaaattaaaaactgatatgtatgaaggacttccattcttttca
 K  I  N  D  W  I  K  L  K  T  D  M  Y  E  G  L  P  F  F  S
aaattgtga
 K  L  -
```

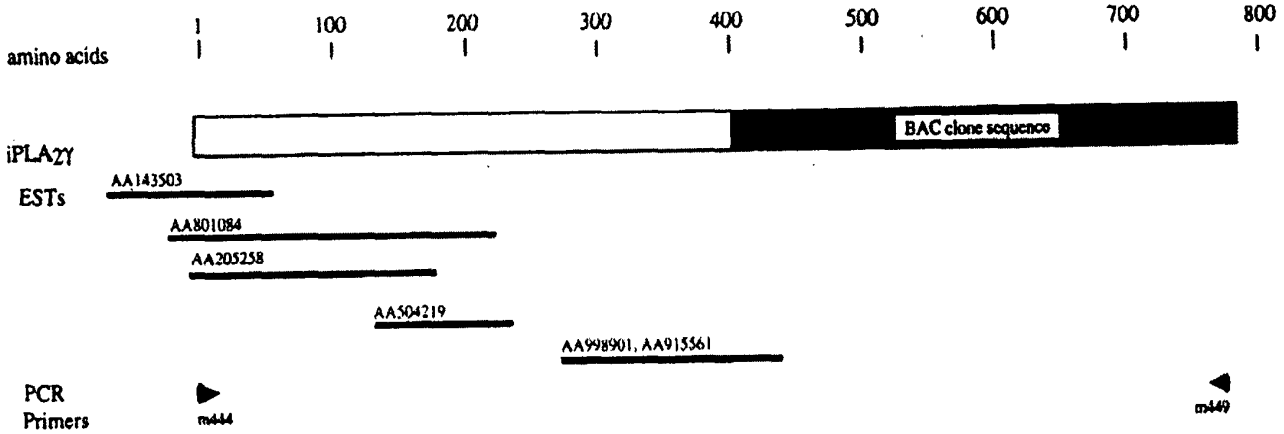

amino acids
1
100
200
300
400
500
600
700
800
iPLA2γ
BAC clone sequence
ESTs
AA143503
AA801084
AA205258
AA504219
AA998901, AA915561
PCR
Primers
m444
m449

Fig. 8

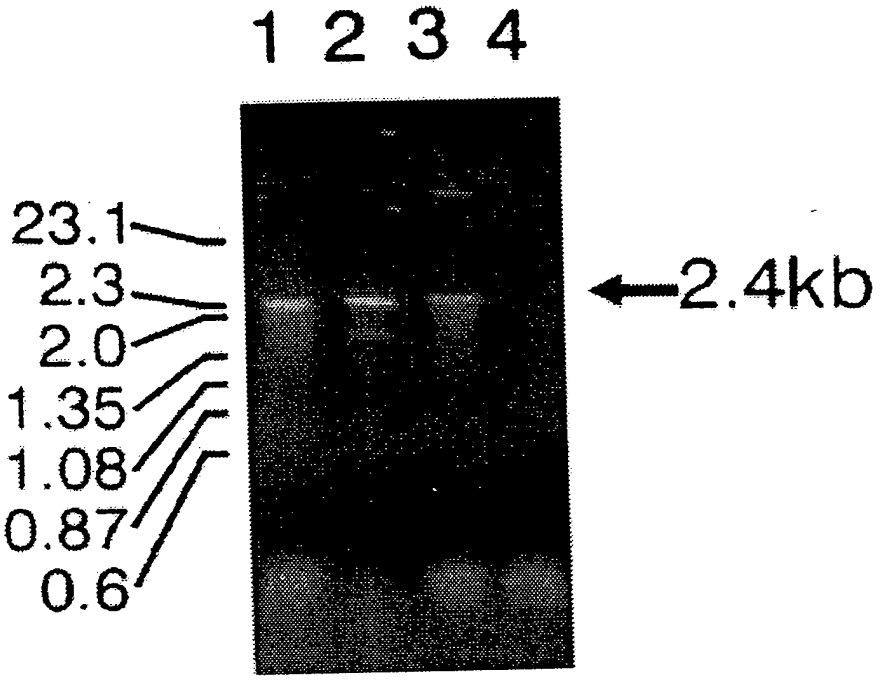


FIG. 9

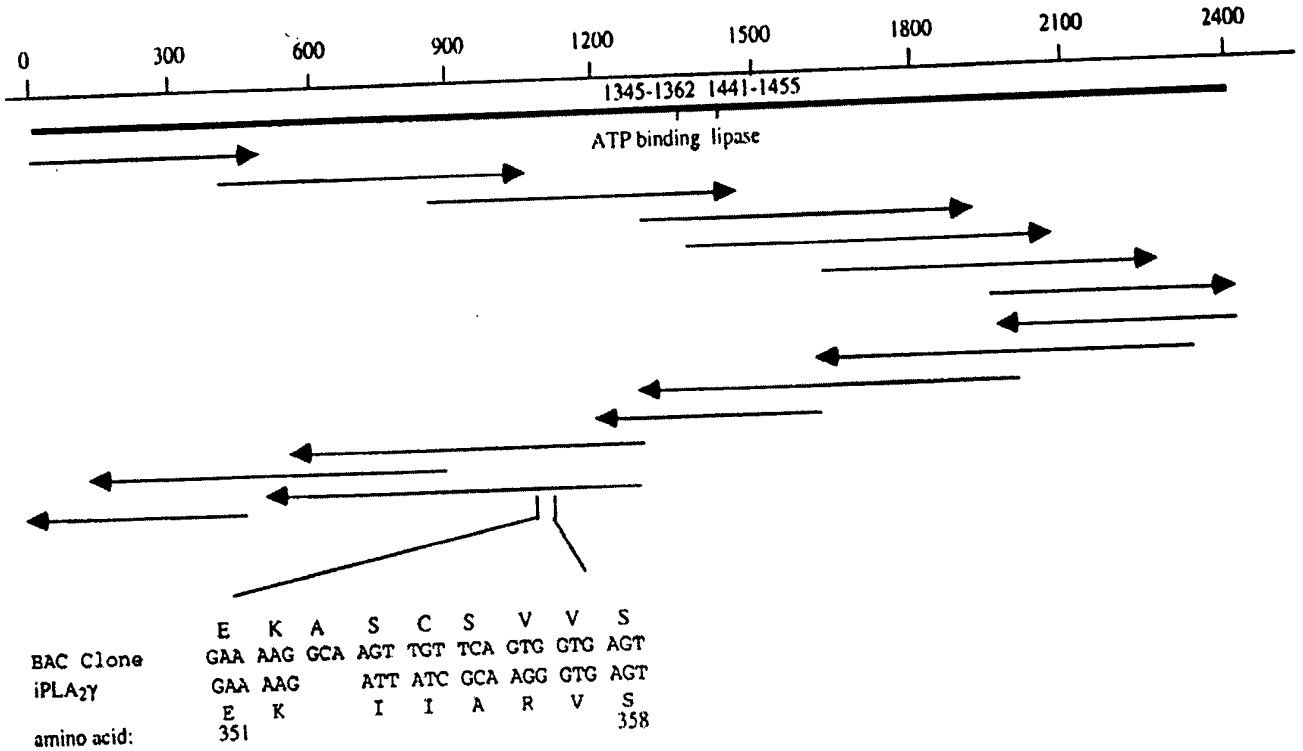
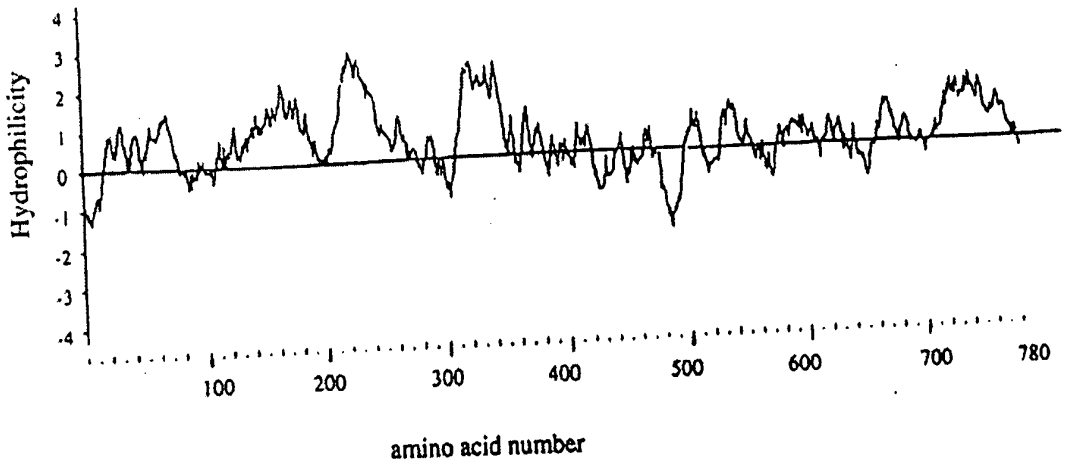

0
300
600
900
1200
1500
1800
2100
2400
1345-1362 1441-1455
ATP binding lipase
E K A S C S V V S
BAC Clone GAA AAG GCA AGT TGT TCA GTG GTG AGT
iPLA2γ GAA AAG ATT ATC GCA AGG GTG AGT
E K I I A R V S
amino acid: 351 358

FIG. 10

FIG. 11


Hydrophilicity
4
3
2
1
0
-1
-2
-3
-4
100
200
300
400
500
600
700
780
amino acid number

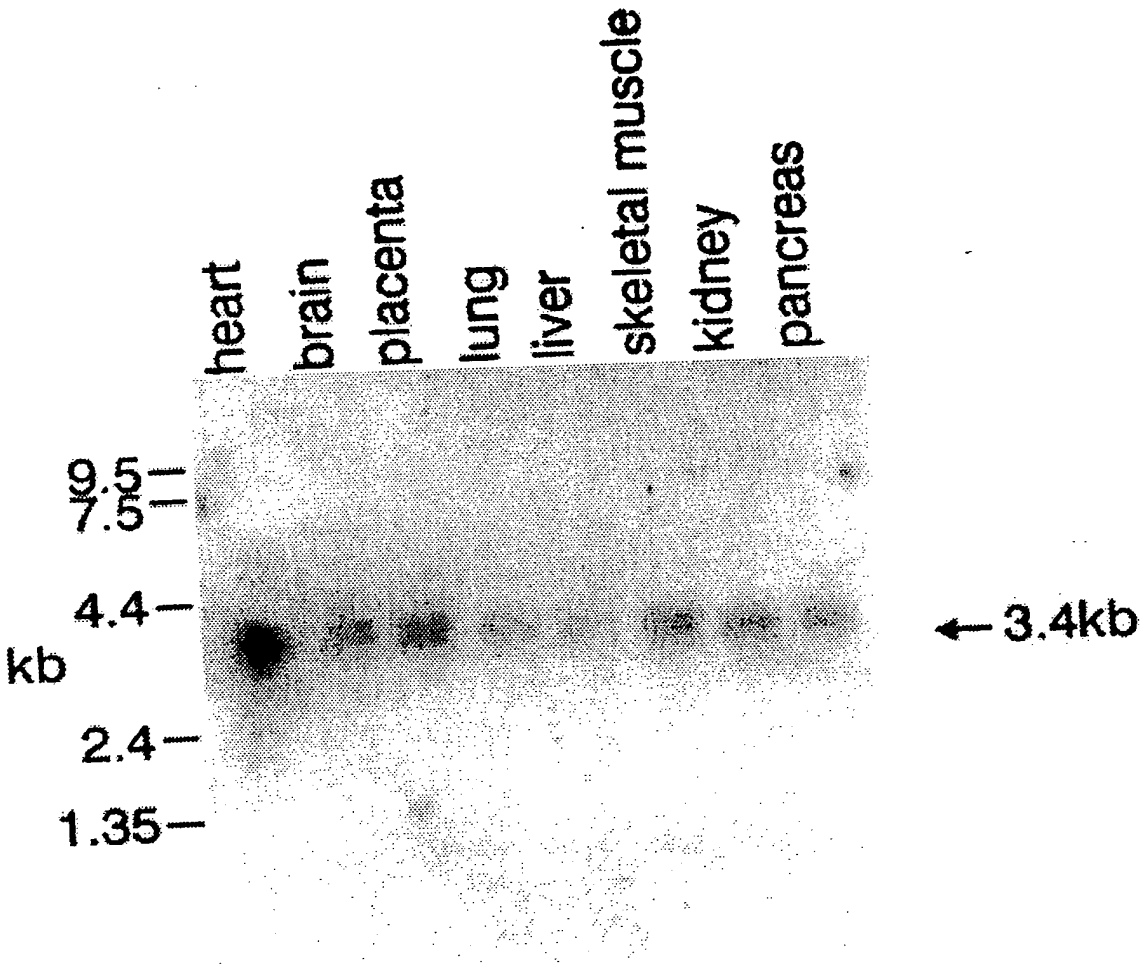

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
9.5
7.5
4.4
kb
2.4
1.35
3.4kb

FIG. 12

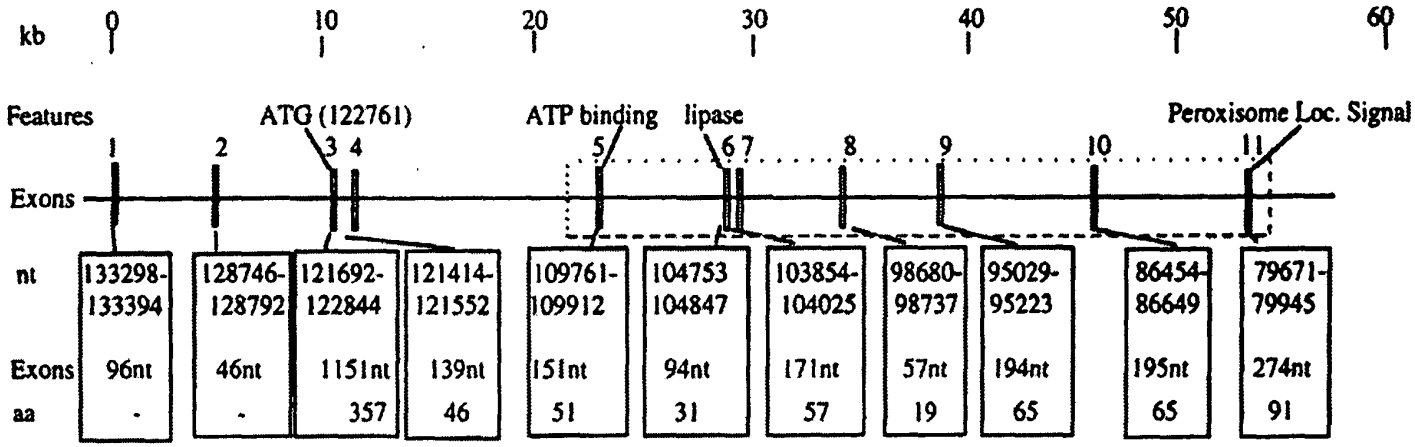

kb
0
10
20
30
40
50
60
Features
ATG (122761)
ATP binding
lipase
Peroxisome Loc. Signal
Exons
1
2
3
4
5
6
7
8
9
10
11
nt
133298-133394
128746-128792
121692-122844
121414-121552
109761-109912
104753 104847
103854-104025
98680-98737
95029-95223
86454-86649
79671-79945
Exons
96nt
46nt
1151nt
139nt
151nt
94nt
171nt
57nt
194nt
195nt
274nt
aa
-
-
357
46
51
31
57
19
65
65
91

FIG. 13

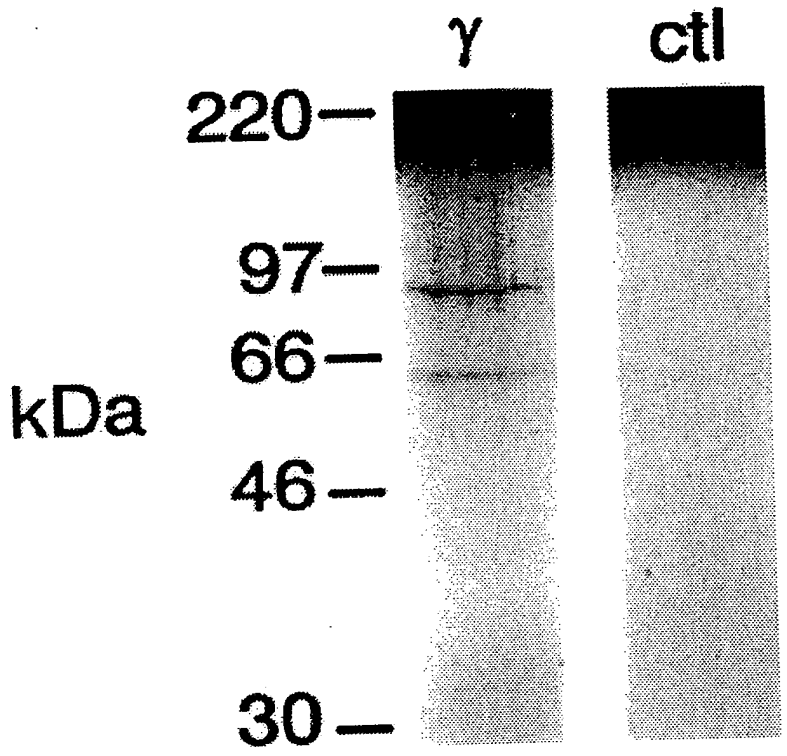


FIG. 14

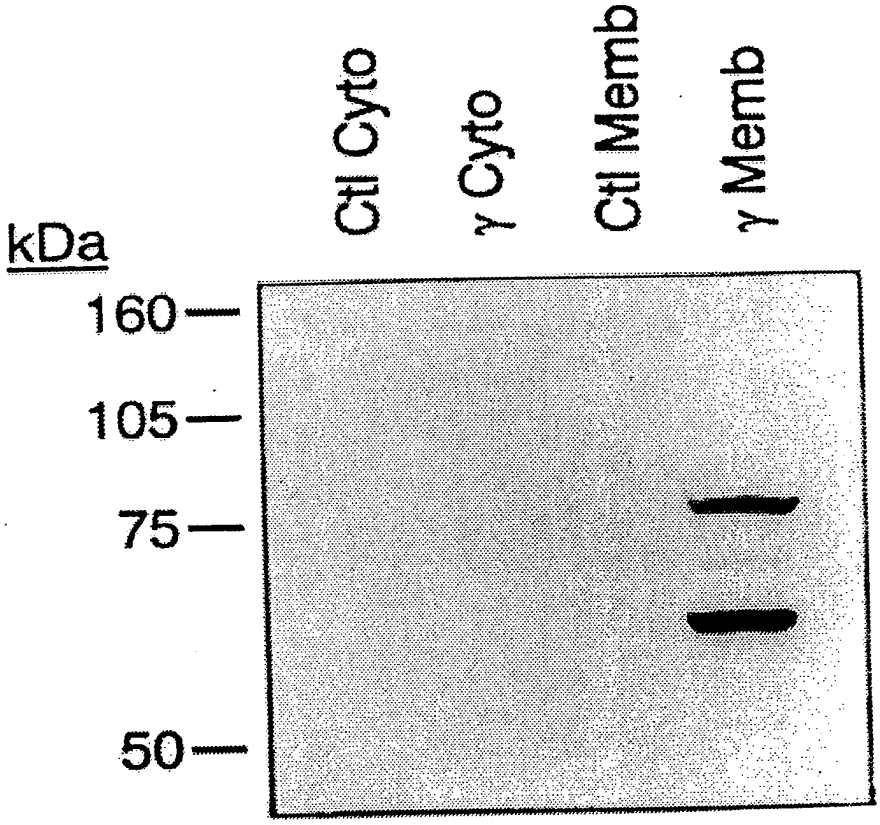


FIG. 15

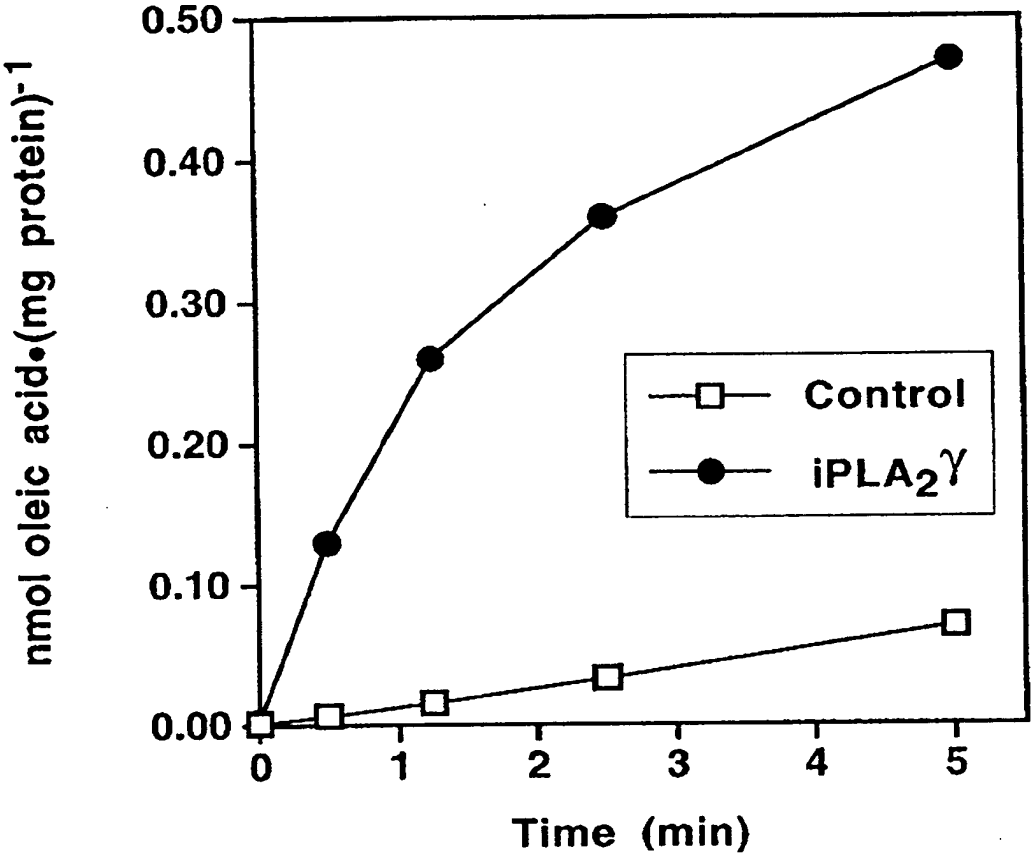

0.50
0.40
0.30
0.20
0.10
0.00
nmol oleic acid•(mg protein)-1
0
1
2
3
4
5
Time (min)
Control
iPLA2γ

FIG. 16

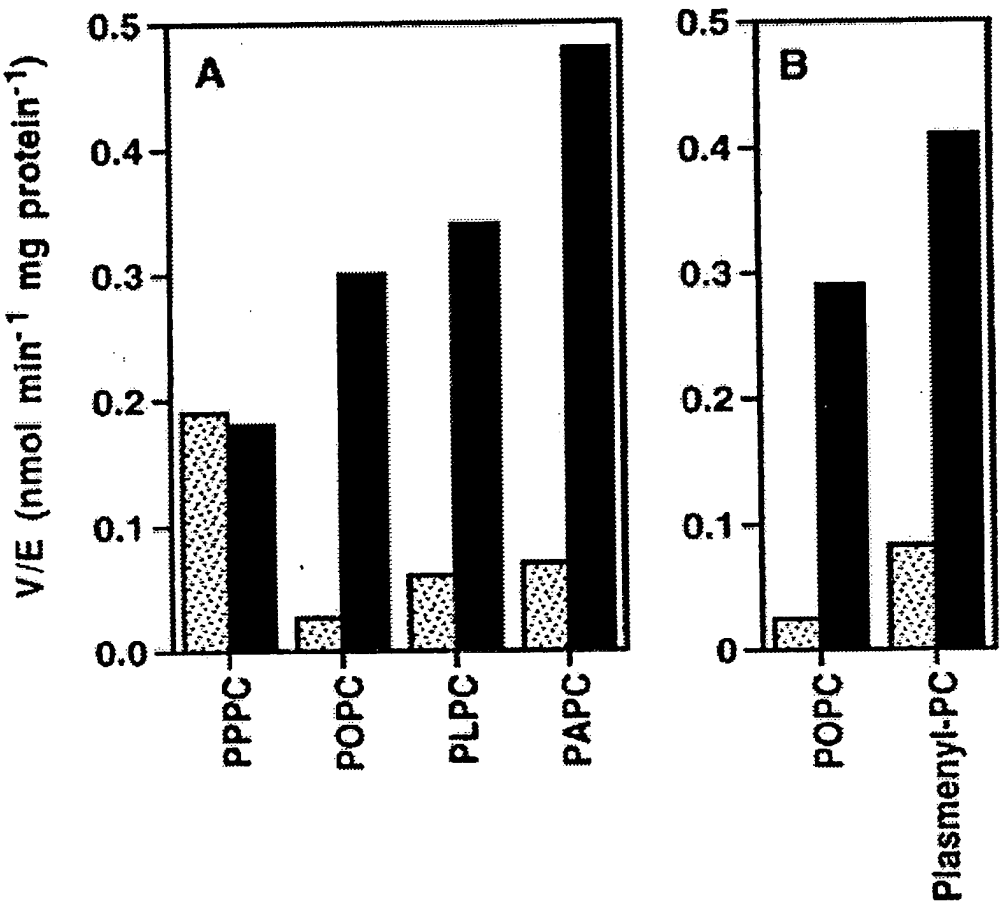

A
B
V/E (nmol min-1 mg protein-1)
0.5
0.4
0.3
0.2
0.1
0.0
0
PPPC
POPC
PLPC
PAPC
POPC
Plasmenyl-PC

FIG. 17

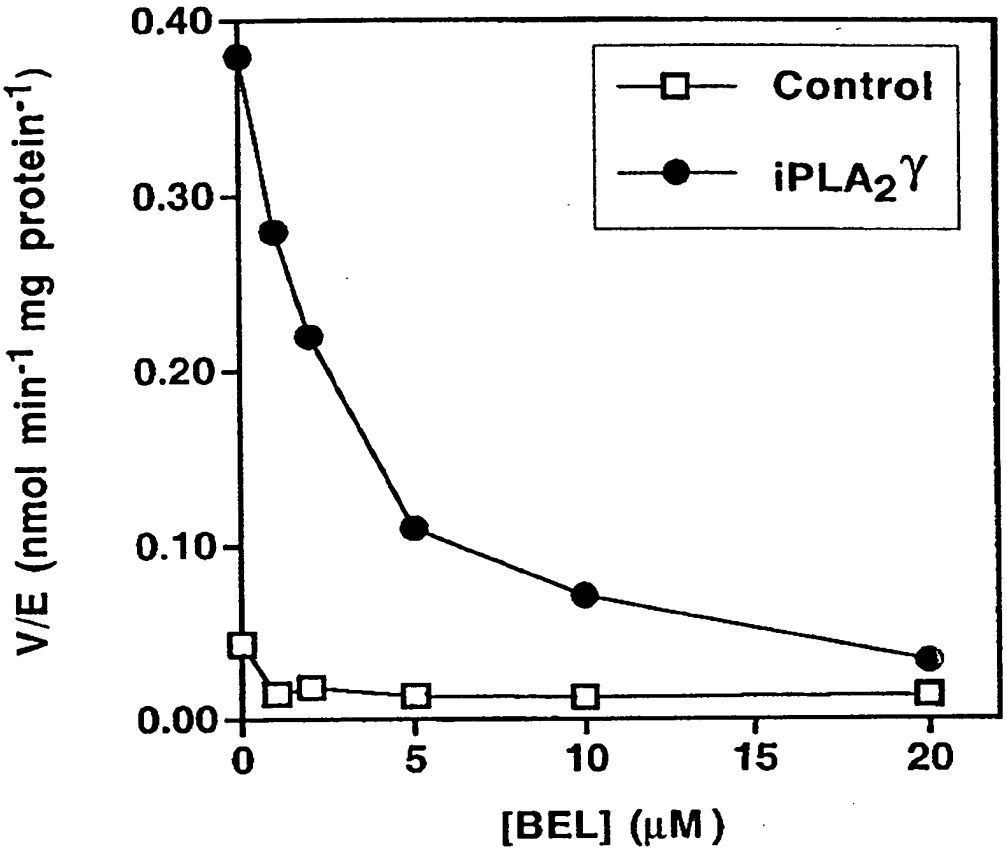

0.40
0.30
0.20
0.10
0.00
V/E (nmol min-1 mg protein-1)
Control
iPLA2γ
0
5
10
15
20
[BEL] (μM)

FIG. 18

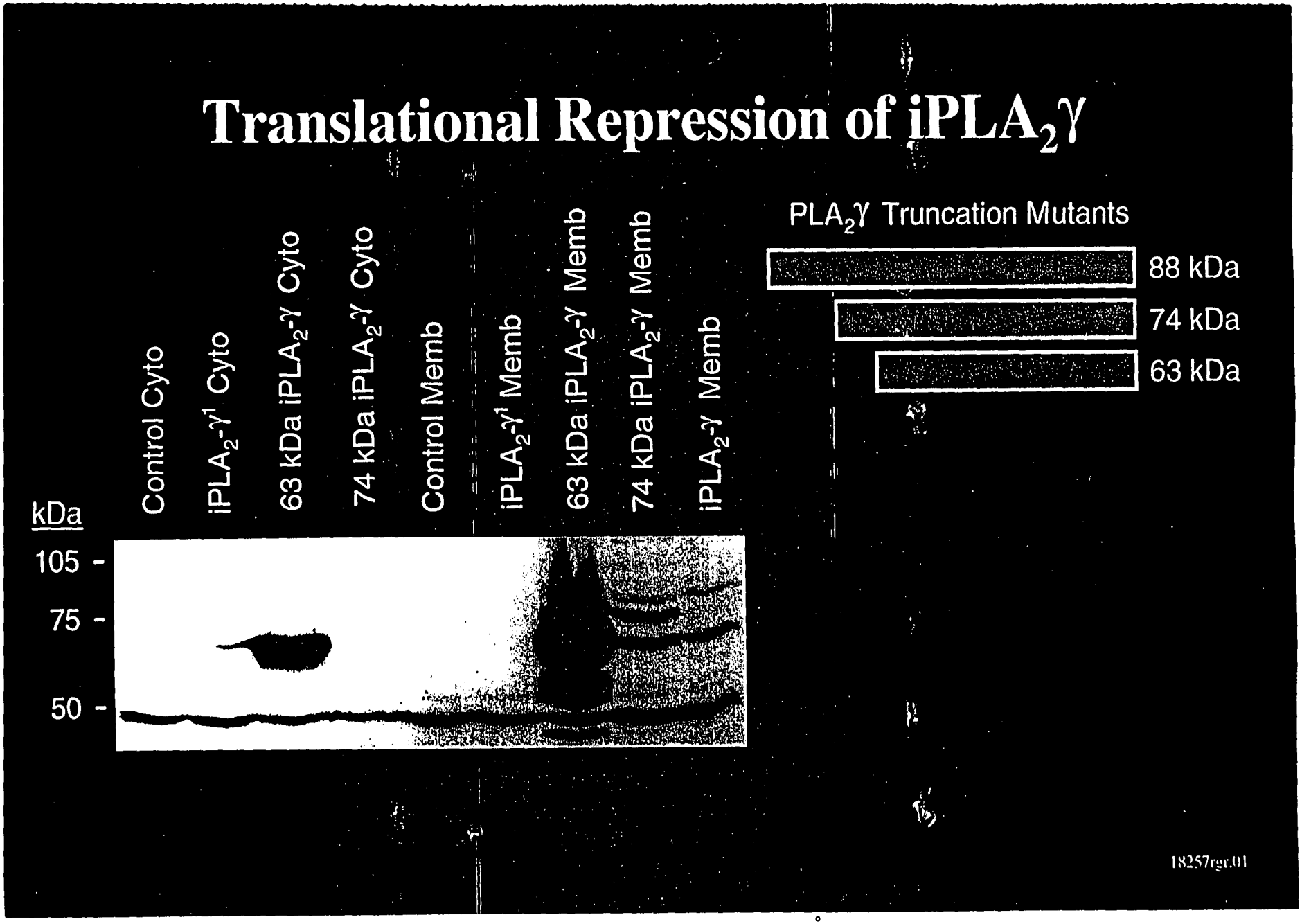

Translational Repression of iPLA2γ
PLA2γ Truncation Mutants
88 kDa
74 kDa
63 kDa
Control Cyto
iPLA2-γ1 Cyto
63 kDa iPLA2-γ Cyto
74 kDa iPLA2-γ Cyto
Control Memb
iPLA2-γ1 Memb
63 kDa iPLA2-γ Memb
74 kDa iPLA2-γ Memb
iPLA2-γ Memb
kDa
105
75
50
18257rgr.01

FIG. 19

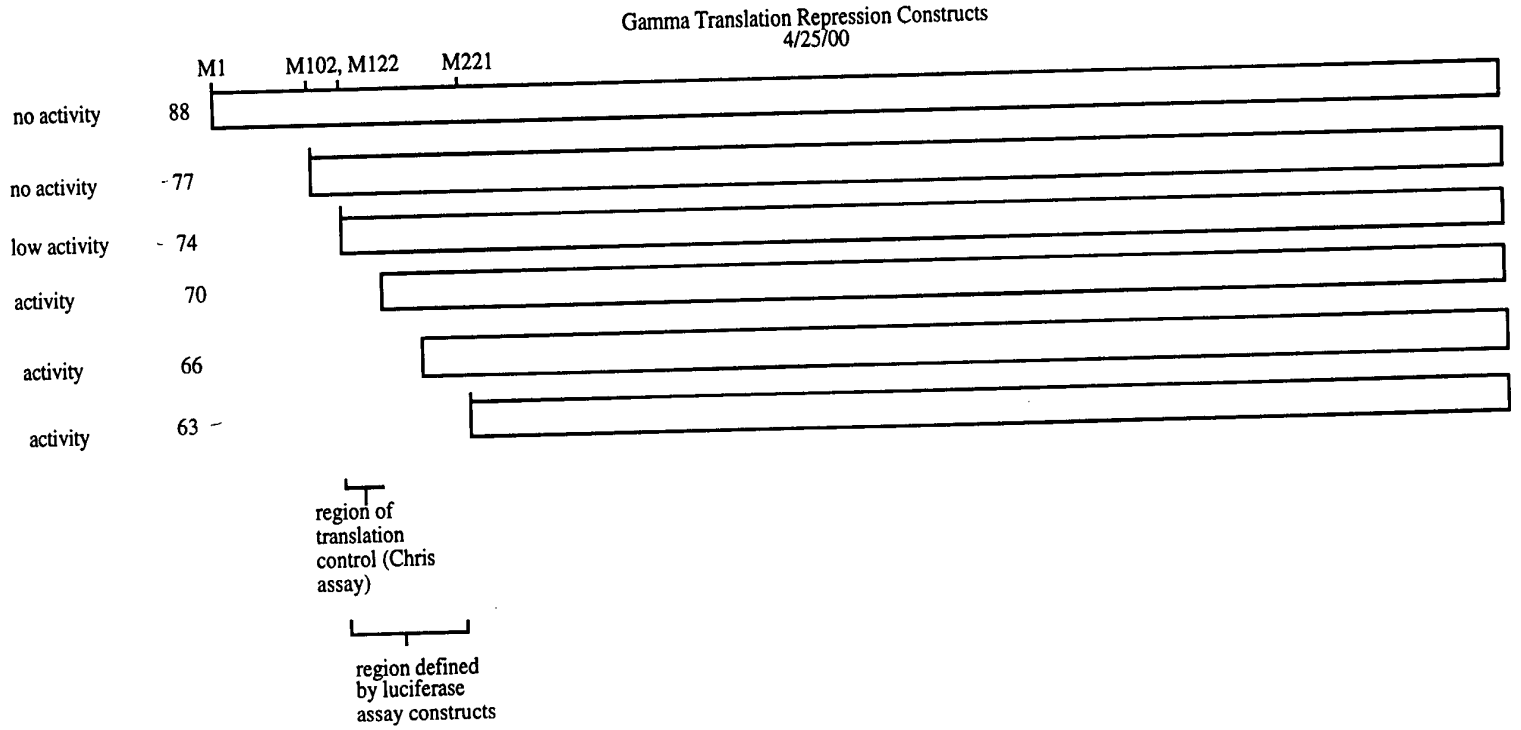

Gamma Translation Repression Constructs
4/25/00
M1
M102, M122
M221
no activity
88
no activity
77
low activity
74
activity
70
activity
66
activity
63
region of translation control (Chris assay)
region defined by luciferase assay constructs

FIG. 20

Ex. 3

Additionally, iPLA2γ sequences were inserted by ligation of 15-23mer annealed phosphorylated oligonucleotide pairs 5' of full-length luciferase coding sequence cloned into pFASTBAC via NotI/XbaI restriction sites and then luciferase activity of recombinant protein produced in the Sf9 system was subsequently measured using the Luciferase Assay System of Promega.

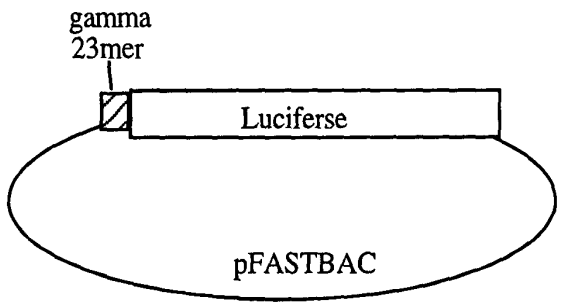


FIG. 21

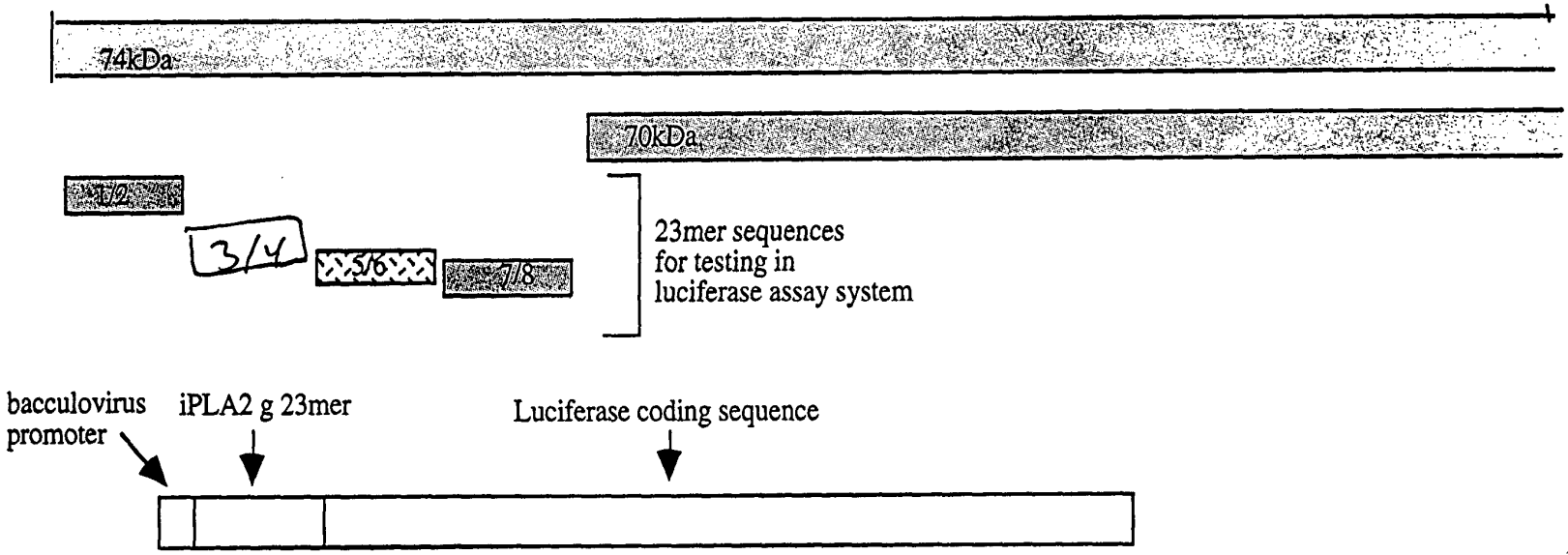

74kDa
70kDa
1/2
3/4
5/6
7/8
23mer sequences
for testing in
luciferase assay system
bacculovirus
promoter
iPLA2 g 23mer
Luciferase coding sequence

FIG. 22

Phosphorylated oligo pairs for sequence between nucleotide 364- 455 for translational repression of iPLA2 gamma in the luciferase expression system:

```
iPLA2γ    atgatttcacgtttagctcaatttaagccaagttcccaaattttaagaaaagtatcggatagtggctggttaaaacagaaaaacatcaaaca
1/2  tcgacctgatttcacgtttagctcaatt
         ggactaaagtgcaaatcgagttaaccgg

3/4                          tcgactaagccaagttcccaaattttaa
                                 gattcggttcaagggtttaaaattccgg

5/6                                                  tcgacgaaaagtatcggatagtggctgg
                                                        gcttttcatagcctatcaccgaccccgg

7/8                                                                          tcgacttaaaacagaaaaacatcaaaca
                                                                                gaattttgtctttttgtagtttgtccgg
```

FIG. 23

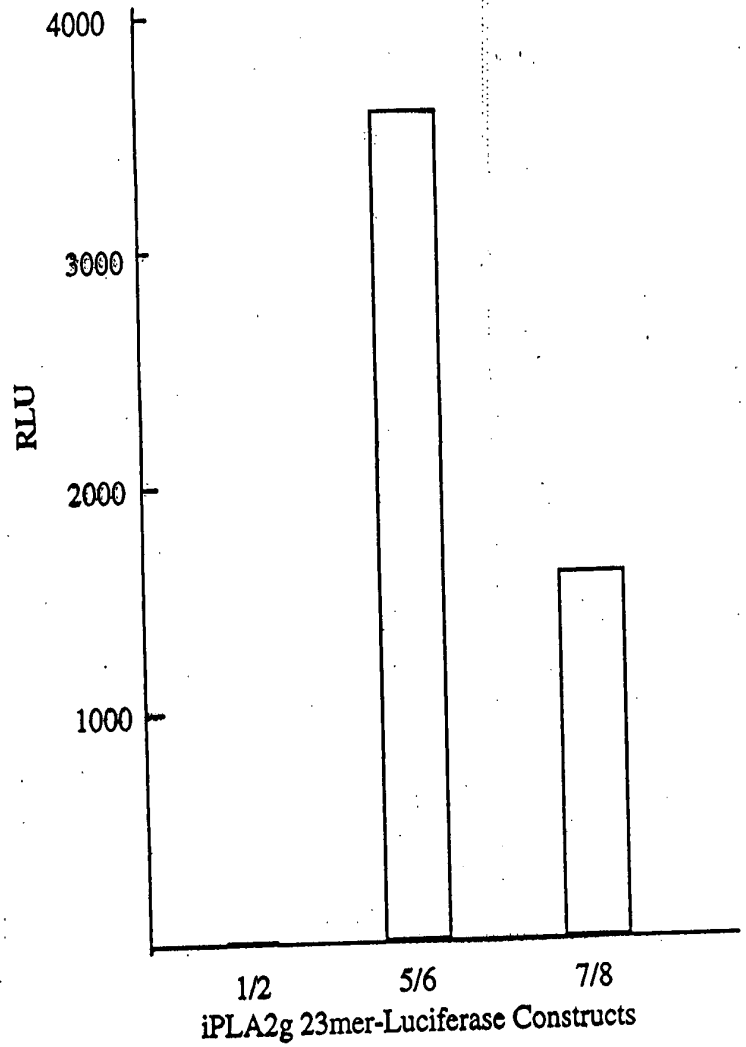

4000
3000
2000
1000
RLU
1/2
5/6
7/8
iPLA2g 23mer-Luciferase Constructs

FIG. 24